

1/10

HPV 45 L1 Nucleotide Sequence Alignment

45 L1 wt	(1)	ATGGCTTTGTGGCGGCCTAGTGACAGTACGGTATATCTTCCACCACCTTC
45 L1 R	(1)A.A..ATC....TC...T..C..CT.G.....A..
45 L1 wt	(51)	TGTGGCCAGAGTTGTCAACACTGATGATTATGTGTCTCGCACAAGCATAT
45 L1 R	(51)	...C..T.....C.....C..C..C..C..CA.A..CTC...C.
45 L1 wt	(101)	TTTACCATGCAGGCAGTTCCCGATTATTAAGTGTAGGCAATCCATATTTT
45 L1 R	(101)	.C.....C..T..TTC....A....G..G.....C..T..C.....C..C
45 L1 wt	(151)	AGGGTTGTACCTAGTGGTGCAGGTAATAAACAGGCTGTTCTAAGGTATC
45 L1 R	(151)	..A..C..C..ATCC.....T.....C..G..A.....A.....C..
45 L1 wt	(201)	CGCATATCAGTATAGGGTGTTTAGAGTAGCTTTGCCCGATCCTAATAAAT
45 L1 R	(201)	T..T..C..A..C..A..C..C.....C.....A..C..A..C..G.
45 L1 wt	(251)	TTGGATTACCTGATTCTACTATATATAATCCTGAAACACAACGTTTGGTT
45 L1 R	(251)	.C..T..G..A..C.....C..C..C..A.....T...A.A.....C
45 L1 wt	(301)	TGGGCATGTGTAGGTATGGAAATTGGTCGTGGGCAGCCTTTAGGTATTGG
45 L1 R	(301)C..C.....C...A.A..T..A..A..G.....C..
45 L1 wt	(351)	CCTAAGTGGCCATCCATTTTATAATAAATTGGATGATACAGAAAGTGCTC
45 L1 R	(351)	TT.GTC...T..C.....C..C..C..G.....C..C..C...TCC....
45 L1 wt	(401)	ATGCAGCTACAGCTGTTATTACGCAGGATGTTAGGGATAATGTGTCAGTT
45 L1 R	(401)	.C..T.....T.....C..C..T..A..C..C..A..C..C..C..T..C
45 L1 wt	(451)	GATTATAAGCAAACACAGCTGTGTATTTTAGGTTGTGTACCTGCTATTGG
45 L1 R	(451)	..C..C.....C..AT.....C..G.....C..A.....C..
45 L1 wt	(501)	TGAGCACTGGGCCAAGGGCACACTTTGTAAACCTGCACAATTGCAACCTG
45 L1 R	(501)	...A.....T.....T..CT.G.....G..A..T.....A.
45 L1 wt	(551)	GTGACTGTCCTCCTTTGGAACCTAAAAACACCATTATTGAGGATGGTGAT
45 L1 R	(551)A..A.....T.G..G.....T..C..C..A..C.....C

FIG.1A

2/10

45 L1 wt	(601)	ATGGTGGATACAGGTTATGGGGCAATGGATTTTAGTACATTGCAGGATAC
45 L1 R	(601)T..C..T.....C..T..T.....C..CTCC..CC.....C..
45 L1 wt	(651)	AAAGTGCAGGTTCCATTAGACATTTGTCAATCCATCTGTAAATATCCAG
45 L1 R	(651)	T.....T..A.....G.....C.....T.....G..C....
45 L1 wt	(701)	ATTATTTGCAAATGTCTGCTGATCCCTATGGGGATTCTATGTTTTTTTGC
45 L1 R	(701)	.C..C.....C.....C..A..C..T..C.....C..C..T
45 L1 wt	(751)	CTACGCCGTGAACAACCTGTTTGCAAGACATTTTGGGAATAGGGCAGGTGT
45 L1 R	(751)	T.GA.AA.A.....T....C..T.....C..C.....C..A..T.....
45 L1 wt	(801)	TATGGGTGACACAGTACCTACAGACCTATATATTAAAGGCACTAGCGCTA
45 L1 R	(801)	C.....T..T..A..T...T.G..C..C..G..T..CTCT....
45 L1 wt	(851)	ATATGCGTGAAACCCCTGGCAGTTGTGTGTATTCCCCTTCTCCCAGTGGC
45 L1 R	(851)	.C...A.A.....T..A..TTCC.....C..C..T..A....ATC...T
45 L1 wt	(901)	TCTATTACTACTTCTGATTCTCAATTATTTAATAAGCCATATTGGTTACA
45 L1 R	(901)C.....C..C.....G..C..C.....C.....G..
45 L1 wt	(951)	TAAGGCCCAGGGCCATAACAATGGTATTTGTTGGCATAATCAGTTGTTTG
45 L1 R	(951)	C.....T..A..T..C.....C.....C.....C..C..A.....C.
45 L1 wt	(1001)	TTACTGTAGTGGACACTACCCGCAGTACTAATTTAACATTATGTGCCTCT
45 L1 R	(1001)	.C..C..C..T.....A.ATC.....C..G..C..G.....T...
45 L1 wt	(1051)	ACACAAAATCCTGTGCCAAATACATATGATCCTACTAAGTTTAAGCACTA
45 L1 R	(1051)	..T.....C..A..T.....C..T..C..C..A..C.....C.....
45 L1 wt	(1101)	TAGTAGACATGTGGAGGAATATGATTTACAGTTTATTTTTCAGTTGTGCA
45 L1 R	(1101)	CTCC.....C..C.....C..C..G..A..C..C..C..A.....T.
45 L1 wt	(1151)	CTATTACTTTAACTGCAGAGGTTATGTCATATATCCATAGTATGAATAGT
45 L1 R	(1151)C..C..G..C..T..A..C.....C..C..T..CTC.....CTCC
45 L1 wt	(1201)	AGTATATTGGAAAATTGGAATTTTGGTGTACCTCCACCACCTACTACAAG
45 L1 R	(1201)	TC...C.....C.....C..C.....T..A.....A..C..CTC

FIG.1B

3/10

45 L1 wt	(1251)	TTTAGTGGATACATATCGTTTTGTGCAATCAGTTGCTGTTACCTGTCAAA
45 L1 R	(1251)	C..G..T..C..T..CA.A..C..C.....T..C.....C..T.....
45 L1 wt	(1301)	AGGATACTACACCTCCAGAAAAGCAGGATCCATATGATAAATTAAAGTTT
45 L1 R	(1301)C..C..T..A.....A..C.....C..C..G..G.....C
45 L1 wt	(1351)	TGGACTGTTGACCTAAAGGAAAAATTTTCCTCCGATTTGGATCAATATCC
45 L1 R	(1351)T.G.....G..C..T.....C.....C.....C..
45 L1 wt	(1401)	CCTTGGTCGAAAGTTTTTAGTTCAGGCTGGGTTACGTCGTAGGCCTACCA
45 L1 R	(1401)	AT.G...A.....C..G.....A.....T..GA.A.....A..A..T.
45 L1 wt	(1451)	TAGGACCTCGTAAGCGTCCTGCTGCTTCCACGTCTACTGCATCTAGGCCT
45 L1 R	(1451)	.C..T..A.....A.A..A.....T..C.....T.....A..A
45 L1 wt	(1501)	GCCAAACGTGTACGTATACGTAGTAAAAAATAA (SEQ ID NO:3)
45 L1 R	(1501)	..T..G.....CA.A..CA.ATCC..G..G...(SEQ ID NO:1)

FIG.1C

4/10

Synthetic HPV 45 L1 Nucleotide and Amino Acid Sequences

M A L W R P S D S T V Y L P P P S
 1 ATGGCTTTGT GGAGACCATC TGA CTCTACT GTCTACTTGC CACCACCATC
 TACCGAAACA CCTCTGGTAG ACTGAGATGA CAGATGAACG GTGGTGGTAG
 V A R V V N T D D Y V S R T S I F
 51 TGTCGCTAGA GTCGTCAACA CTGACGACTA CGTCTCCAGA ACCTCCATCT
 ACAGCGATCT CAGCAGTTGT GACTGCTGAT GCAGAGGTCT TGGAGGTAGA
 Y H A G S S R L L T V G N P Y F
 101 TCTACCACGC TGGTTCTTCC AGATTGTTGA CTGTGGGTAA CCCATACTTC
 AGATGGTGCG ACCAAGAAGG TCTAACAAC T GACAGCCATT GGGTATGAAG
 R V V P S G A G N K Q A V P K V S
 151 AGAGTCGTCC CATCCGGTGC TGGTAACAAG CAAGCTGTTC CAAAGGTCTC
 TCTCAGCAGG GTAGGCCACG ACCATTGTTC GTTCGACAAG GTTTCAGAG
 A Y Q Y R V F R V A L P D P N K F
 201 TGCTTACCAA TACAGAGTCT TCAGAGTCGC TTTGCCAGAC CCAAACAAGT
 ACGAATGGTT ATGTCTCAGA AGTCTCAGCG AAACGGTCTG GGTTTGTTC A
 G L P D S T I Y N P E T Q R L V
 251 TCGGTTTGCC AGACTCTACT ATCTACAACC CAGAAACTCA AAGATTGGTC
 AGCCAAACGG TCTGAGATGA TAGATGTTGG GTCTTTGAGT TTCTAACCAG
 W A C V G M E I G R G Q P L G I G
 301 TGGGCATGCG TCGGTATGGA AATCGGTAGA GGTCAACCAT TGGGTATCGG
 ACCCGTACGC AGCCATACCT TTAGCCATCT CCAGTTGGTA ACCCATAGCC
 L S G H P F Y N K L D D T E S A H
 351 TTTGTCTGGT CACCCATTCT ACAACAAGTT GGACGACACC GAATCCGCTC
 AAACAGACCA GTGGGTAAGA TGTTGTTCAA CCTGCTGTGG CTTAGGCGAG
 A A T A V I T Q D V R D N V S V
 401 ACGCTGCTAC TGCTGTCATC ACTCAAGACG TCAGAGACAA CGTCTCTGTC
 TGCGACGATG ACGACAGTAG TGAGTTCTGC AGTCTCTGTT GCAGAGACAG
 D Y K Q T Q L C I L G C V P A I G
 451 GACTACAAGC AAACCCAATT GTGTATCTTG GGTTGTGTCC CAGCTATCGG
 CTGATGTTCG TTTGGGTAA CACATAGAAC CCAACACAGG GTCGATAGCC
 E H W A K G T L C K P A Q L Q P G
 501 TGAACACTGG GCTAAGGGTA CTTGTGTAA GCCAGCTCAA TTGCAACAGG
 ACTTGTGACC CGATTCCCAT GGAACACATT CGGTCGAGTT AACGTTGGTC

FIG.2A

5/10

D C P P L E L K N T I I E D G D
551 GTGACTGTCC ACCATTGGAA TTGAAGAACA CTATCATCGA AGACGGTGAC
CACTGACAGG TGGTAACCTT AACTTCTTGT GATAGTAGCT TCTGCCACTG
M V D T G Y G A M D F S T L Q D T
601 ATGGTTGACA CTGGTTACGG TGCTATGGAC TTCTCCACCC TGCAGGACAC
TACCAACTGT GACCAATGCC ACGATACCTG AAGAGGTGGG ACGTCCTGTG
K C E V P L D I C Q S I C K Y P D
651 TAAGTGTGAA GTTCCATTGG ACATCTGTCA ATCTATCTGT AAGTACCCAG
ATTCACACTT CAAGGTAACC TGTAGACAGT TAGATAGACA TTCATGGGTC
Y L Q M S A D P Y G D S M F F C
701 ACTACTTGCA AATGTCCGCT GACCCATACG GTGACTCTAT GTTCTTCTGT
TGATGAACGT TTACAGGCGA CTGGGTATGC CACTGAGATA CAAGAAGACA
L R R E Q L F A R H F W N R A G V
751 TTGAGAAGAG AACAAATTGTT CGCTAGACAC TTCTGGAACA GAGCTGGTGT
AACTCTTCTC TTGTTAACAA GCGATCTGTG AAGACCTTGT CTCGACCACA
M G D T V P T D L Y I K G T S A N
801 CATGGGTGAC ACTGTTCCAA CTGACTTGTA CATCAAGGGT ACCTCTGCTA
GTACCCACTG TGACAAGGTT GACTGAACAT GTAGTTCCCA TGGAGACGAT
M R E T P G S C V Y S P S P S G
851 ACATGAGAGA AACTCCAGGT TCCTGTGTCT ACTCTCCATC TCCATCTGGT
TGTA CTCTCT TTGAGGTCCA AGGACACAGA TGAGAGGTAG AGGTAGACCA
S I T T S D S Q L F N K P Y W L H
901 TCTATCACTA CTTCCGACTC TCAATTGTTT AACAAAGCCAT ACTGGTTGCA
AGATAGTGAT GAAGGCTGAG AGTTAACAAG TTGTTCCGGTA TGACCAACGT
K A Q G H N N G I C W H N Q L F V
951 CAAGGCTCAA GGTCACAACA ACGGTATCTG TTGGCACAAC CAATTGTTCTG
GTTCCGAGTT CCAGTGTTGT TGCCATAGAC AACCGTGTTG GTTAACAAGC
T V V D T T R S T N L T L C A S
1001 TCACCGTCGT TGACACTACC AGATCTACTA ACTTGACCTT GTGTGCTTCT
AGTGGCAGCA ACTGTGATGG TCTAGATGAT TGAAGTGGAA CACACGAAGA
T Q N P V P N T Y D P T K F K H Y
1051 ACTCAA AACC CAGTTCCAAA CACTTACGAC CCAACCAAGT TCAAGCACTA
TGAGTTTTGG GTCAAGGTTT GTGAATGCTG GGTGGTTCA AGTTCGTGAT
S R H V E E Y D L Q F I F Q L C T
1101 CTCCAGACAC GTCGAGGAAT ACGACTTGCA ATTCATCTTC CAATTGTGTA
GAGGTCTGTG CAGCTCCTTA TGCTGAACGT TAAGTAGAAG GTTAACACAT
I T L T A E V M S Y I H S M N S
1151 CTATCACCTT GACCGCTGAA GTCATGTCCT ACATTCACCTC TATGAACTCC
GATAGTGGAA CTGGCGACTT CAGTACAGGA TGTAAGTGAG ATACTTGAGG

FIG.2B

6/10

S I L E N W N F G V P P P P T T S
1201 TCTATCTTGG AAAACTGGAA CTTCGGTGTT CCACCACCAC CAACCACCTC
AGATAGAACC TTTTGACCTT GAAGCCACAA GGTGGTGGTG GTTGGTGGAG
L V D T Y R F V Q S V A V T C Q K
1251 CTTGGTTGAC ACTTACAGAT TCGTCCAATC TGTCGCTGTC ACTTGTCAAA
GAACCAACTG TGAATGTCTA AGCAGGTTAG ACAGCGACAG TGAACAGTTT
D T T P P E K Q D P Y D K L K F
1301 AGGACACCAC TCCACCAGAA AAGCAAGACC CATACGACAA GTTGAAGTTC
TCCTGTGGTG AGGTGGTCTT TTCGTTCTGG GTATGCTGTT CAACTTCAAG
W T V D L K E K F S S D L D Q Y P
1351 TGGACTGTTG ACTTGAAGGA AAAGTTCTCT TCCGACTTGG ACCAATACCC
ACCTGACAAC TGAACCTCCT TTTCAAGAGA AGGCTGAACC TGGTTATGGG
L G R K F L V Q A G L R R R P T I
1401 ATTGGGTAGA AAGTTCTTGG TTCAAGCTGG TTTGAGACGT AGACCAACTA
TAACCCATCT TTCAAGAACC AAGTTCGACC AAACCTGCA TCTGGTTGAT
G P R K R P A A S T S T A S R P
1451 TCGGTCCACG TAAGAGACCA GCTGCTTCCA CTTCCACTGC TTCTAGACCA
AGCCAGGTGC ATTCTCTGGT CGACGAAGGT GAAGGTGACG AAGATCTGGT
A K R V R I R S K K * (SEQ ID NO:2)
1501 GCTAAGCGTG TCAGAATCAG ATCCAAGAAG TAA (SEQ ID NO:1)
CGATTGCGAC AGTCTTAGTC TAGGTTCTTC ATT (SEQ ID NO:8)

FIG.2C

7/10

NORTHERN BLOT ANALYSIS OF HPV 45 L1 R.

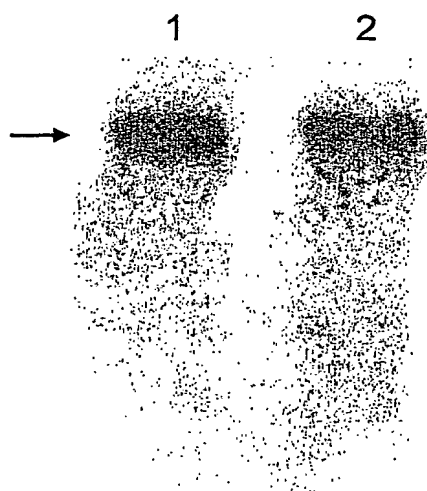


FIG.3

8/10

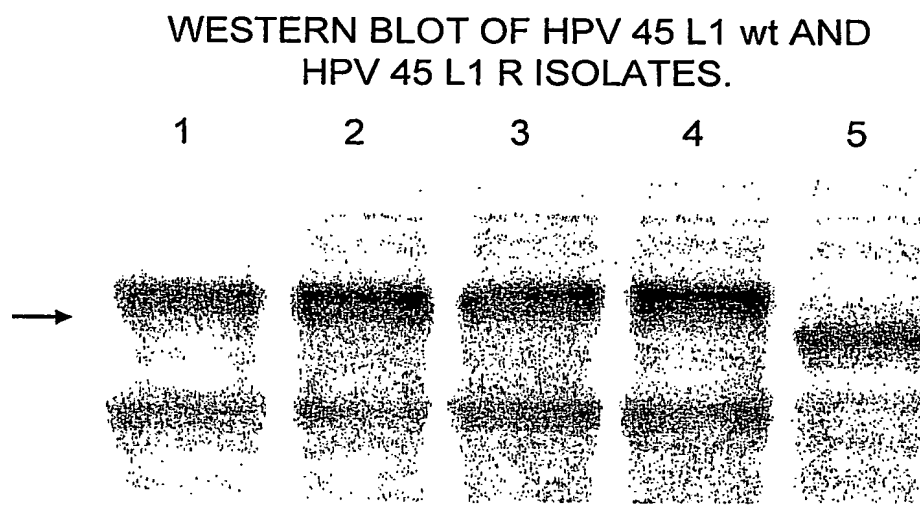


FIG.4

ELISA ASSAY

L1 CONSTRUCT	ng VLP/mcg TOTAL PROTEIN	FOLD INCREASE OVER WILD--TYPE
45 L1 WILD--TYPE	5 ng VLP/mcg TOTAL PROTEIN	na
45 L1 ISOLATE #4	12 ng VLP/mcg TOTAL PROTEIN	2.4
45 L1 R ISOLATE #11	10 ng VLP/mcg TOTAL PROTEIN	2.0

FIG.5

10/10

TRANSMISSION EM OF VLPs COMPOSED OF HPV
45 L1 R PROTEIN MOLECULES.

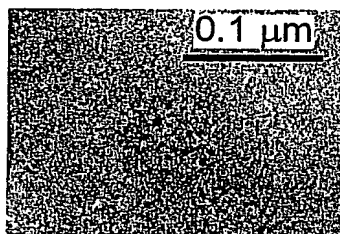


FIG.6